



SEQUENCE LISTING

<110> Anderson, Annaliesa S.
 Jansen, Kathrin Ute
 Kelly, Rosemarie
 Schultz, Loren D.
 Montgomery, Donna L.
 McClements, William L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE
 IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569YP

<140> US 10/564,458

<141> 2006-01-12

<150> PCT/2004/023523

<151> 2004-07-22

<150> 60/489,840

<151> 2003-07-24

<150> 60/520,115

<151> 2003-11-14

<160> 109

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI with amino terminus methionine

<400> 1

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		20						25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala
		35				40						45			
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala
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Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn
65				70				75						80	
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro
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Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp
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Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
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Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
    130                135                140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
    145                150                155                160
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
                165                170                175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
                180                185                190
Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys
    195                200                205
Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
    210                215                220
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
    225                230                235                240
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
                245                250                255
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
                260                265                270
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
    275                280                285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
    290                295                300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
    305                310                315                320
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
                325                330                335
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
    340                345                350
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
    355                360                365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
    370                375                380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
    385                390                395                400
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
                405                410                415
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
    420                425                430
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
    435                440                445

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<210> 2
 <211> 645
 <212> PRT
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<400> 2
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    20                25                30

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Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Ala	Glu	Glu	Thr	Gly	Gly	Thr	
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Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	
	50					55					60					
Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	
65					70					75					80	
Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	
			85						90					95		
Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	
			100					105					110			
Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	
		115					120					125				
Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	
	130					135					140					
Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	
145					150					155					160	
Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	
				165					170					175		
Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	
			180					185					190			
Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	
		195					200					205				
Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	
	210					215					220					
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	
225					230					235					240	
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	
				245					250					255		
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	
			260					265					270			
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	
		275					280					285				
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	
	290					295					300					
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	
305					310					315					320	
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	
				325					330					335		
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	
		340						345					350			
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	
		355					360					365				
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	
	370					375					380					
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	
385					390					395					400	
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	
				405					410					415		
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	
			420					425					430			
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	
		435					440					445				
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	
	450					455					460					

Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	
465					470					475						480
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	
				485					490						495	
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	
			500					505					510			
Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	
		515					520					525				
Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	
	530					535						540				
Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	
545					550					555					560	
Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	
			565					570						575		
Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	
			580					585					590			
His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	
		595					600					605				
Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	
	610				615						620					
Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	
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Arg	Lys	Arg	Lys	Asn												
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<210> 3

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine

<400> 3

Met	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	
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Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	
			20					25					30			
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	
		35				40						45				
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	
	50					55					60					
Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	
65				70					75					80		
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	
			85					90					95			
Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	
			100					105					110			
Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	
	115						120					125				
Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	
	130					135					140					
Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	
145					150					155					160	

Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	
				165					170					175		
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	
			180					185					190			
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	
			195				200					205				
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	
	210					215					220					
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	
225					230					235					240	
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	
				245					250					255		
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	
			260					265					270			
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	
			275				280					285				
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	
	290					295					300					
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	
305					310					315					320	
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	
			325					330						335		
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	
			340					345					350			
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	
			355				360					365				
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	
	370					375					380					
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	
385					390					395					400	
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	
				405					410					415		
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	
			420					425					430			
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	
		435					440					445				
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	
	450					455					460					
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	
465					470					475					480	
Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	
				485					490					495		
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	
			500					505					510			
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	
		515					520					525				
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	
	530					535					540					
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	
545					550					555					560	
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
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<210> 4
 <211> 570
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH with amino terminus methionine-glycine

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 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
 35 40 45
 Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
 50 55 60
 Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
 65 70 75 80
 Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
 85 90 95
 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
 100 105 110
 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
 115 120 125
 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
 130 135 140
 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
 145 150 155 160
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
 165 170 175
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
 180 185 190
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
 195 200 205
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
 210 215 220
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
 225 230 235 240
 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
 245 250 255
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
 260 265 270
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
 275 280 285
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
 290 295 300
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
 305 310 315 320
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
 325 330 335
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
 340 345 350
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
 355 360 365

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Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
 370          375          380
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
385          390          395          400
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
          405          410          415
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
          420          425          430
Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser
          435          440          445
Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn
          450          455          460
Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser
465          470          475          480
Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu
          485          490          495
Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val
          500          505          510
Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln
          515          520          525
Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys
          530          535          540
Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn
545          550          555          560
Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 5

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine-glycine

<400> 5

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Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys
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Thr Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu
          20          25          30
Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
          35          40          45
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
          50          55          60
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
65          70          75          80
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
          85          90          95
Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
          100          105          110
Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
          115          120          125
Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
130          135          140

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Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
 145 150 155 160
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
 165 170 175
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
 180 185 190
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
 195 200 205
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
 210 215 220
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
 225 230 235 240
 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
 245 250 255
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
 260 265 270
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
 275 280 285
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
 290 295 300
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
 305 310 315 320
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
 325 330 335
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
 340 345 350
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
 355 360 365
 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
 370 375 380
 Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
 385 390 395 400
 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
 405 410 415
 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
 420 425 430
 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
 435 440 445

<210> 6

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 6

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
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 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
 20 25 30
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
 35 40 45

Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	
50						55					60					
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	
65					70					75					80	
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	
				85					90					95		
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	
			100					105					110			
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	
		115					120						125			
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	
	130					135					140					
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	
145					150					155					160	
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	
				165					170					175		
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	
			180					185					190			
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	
		195					200					205				
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	
	210					215					220					
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	
225					230					235					240	
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	
				245					250					255		
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	
			260					265					270			
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	
		275					280					285				
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	
	290					295					300					
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	
305					310					315					320	
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Ala	Phe	Val	Lys	His	
				325					330					335		
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	
			340					345					350			
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	
		355					360					365				
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	
	370					375					380					
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	
385					390					395					400	
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	
				405					410					415		
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys	
			420					425					430			
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro	
		435					440					445				
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	
	450					455					460					
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	
465					470					475					480	

```

Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
      485                      490          495
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
      500                      505          510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
      515                      520          525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
      530                      535          540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545                      550          555          560
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
      565                      570          575

```

```

<210> 7
<211> 568
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> ORF0657nH

```

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<400> 7
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
 20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
 35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50      55      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
 65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
 85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
 100     105     110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
 115     120     125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
 130     135     140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
 145     150     155     160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
 165     170     175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
 180     185     190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195     200     205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210     215     220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225     230     235     240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245     250     255

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Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260                265                270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
275                280                285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290                295                300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305                310                315
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
325                330                335
Gly Lys Lys Tyr Met Val Met Glu Thr Asn Asp Asp Tyr Trp Lys
340                345                350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
355                360                365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
370                375                380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                390                395
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
405                410                415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
420                425                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
435                440                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
450                455                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                470                475
Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
485                490                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
500                505                510
Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
515                520                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                535                540
Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                550                555
Thr Gln Glu Asn Lys Ala Lys Ser
565

```

<210> 8

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 8

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
20          25          30

```

Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys									

```

Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465          470          475          480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
          485          490          495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
          500          505          510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
          515          520          525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
          530          535          540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545          550          555          560
Thr Gln Glu Asn Lys Ala Lys Ser
          565

```

```

<210> 9
<211> 568
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> ORF0657nH

```

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<400> 9
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
          20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
          50          55          60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195          200          205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210          215          220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225          230          235          240

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Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
      245      250      255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
      260      265      270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
      275      280      285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
      290      295      300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305      310      315      320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
      325      330      335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340      345      350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
      355      360      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370      375      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385      390      395      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405      410      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
450      455      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465      470      475      480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
      500      505      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545      550      555      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

```

```

<210> 10
<211> 568
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> ORF0657nH

```

```

<400> 10
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15

```

Ala	Val	Ala	Ser 20	Pro	Thr	Thr	Thr	Ser 25	Glu	Lys	Ala	Pro	Glu 30	Thr	Lys
Pro	Val	Ala 35	Asn	Ala	Val	Ser	Val	Ser 40	Asn	Lys	Glu	Val 45	Glu	Ala	Pro
Thr	Ser 50	Glu	Thr	Lys	Glu	Ala 55	Lys	Glu	Val	Lys	Glu 60	Val	Lys	Ala	Pro
Lys 65	Glu	Thr	Lys	Glu	Val 70	Lys	Pro	Ala	Ala	Lys 75	Ala	Thr	Asn	Asn	Thr 80
Tyr	Pro	Ile	Leu	Asn 85	Gln	Glu	Leu	Arg	Glu 90	Ala	Ile	Lys	Asn	Pro	Ala
Ile	Lys	Asp	Lys 100	Asp	His	Ser	Ala	Pro 105	Asn	Ser	Arg	Pro	Ile 110	Asp	Phe
Glu	Met 115	Lys	Lys	Lys	Asp	Gly	Thr 120	Gln	Gln	Phe	Tyr	His 125	Tyr	Ala	Ser
Ser	Val 130	Lys	Pro	Ala	Arg	Val 135	Ile	Phe	Thr	Asp	Ser 140	Lys	Pro	Glu	Ile
Glu 145	Leu	Gly	Leu	Gln	Ser 150	Gly	Gln	Phe	Trp	Arg 155	Lys	Phe	Glu	Val	Tyr 160
Glu	Gly	Asp	Lys 165	Lys	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly 190	Thr	Lys	Ala
Val	Lys 195	Ile	Val	Ser	Ser	Thr	His 200	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr 220	Asn	Ser	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu	Glu 230	Asp	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ala	Pro 240
Tyr	Lys	Lys	Ala 245	Lys	Thr	Leu	Glu	Arg	Gln 250	Val	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr 270	Lys	Lys	Lys
Leu	Glu	Asp 275	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
Thr	Glu 290	Phe	Gln	Lys	Val	Gln 295	Pro	Thr	Asn	Glu	Lys 300	Met	Thr	Asp	Leu
Gln 305	Asp	Thr	Lys	Tyr	Val 310	Val	Tyr	Glu	Ser	Val 315	Glu	Asn	Asn	Glu	Ser 320
Met	Met	Asp	Thr 325	Phe	Val	Lys	His	Pro	Ile 330	Lys	Thr	Gly	Met	Leu 335	Asn
Gly	Lys	Lys	Tyr 340	Met	Val	Met	Glu	Thr 345	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe 355	Met	Val	Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys	Asn 370	Asn	Thr	Arg	Thr	Ile 375	Ile	Phe	Pro	Tyr	Val 380	Glu	Gly	Lys	Thr
Leu 385	Tyr	Asp	Ala	Ile	Val 390	Lys	Val	His	Val	Lys 395	Thr	Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His 405	Val	Arg	Ile	Val	Asp	Lys 410	Glu	Ala	Phe	Thr	Lys 415	Ala
Asn	Thr	Asp 420	Lys	Ser	Asn	Lys	Lys	Glu 425	Gln	Gln	Asp	Asn	Ser 430	Ala	Lys
Lys	Glu	Ala 435	Thr	Pro	Ala	Thr	Pro 440	Ser	Lys	Pro	Thr	Pro 445	Ser	Pro	Val

```

Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
  450                      455                      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
  465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                      530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
  545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

```

```

<210> 11
<211> 565
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> ORF0657nH

```

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<400> 11
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
                      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
                      50                      55                      60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile
  65                      70                      75                      80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
                      85                      90                      95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
                      100                      105                      110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
                      115                      120                      125
Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly
                      130                      135                      140
Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp
  145                      150                      155                      160
Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr
                      165                      170                      175
Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile
                      180                      185                      190
Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr
                      195                      200                      205
Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys
  210                      215                      220

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```

Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys
225          230          235          240
Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp
          245          250          255
Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp
          260          265          270
Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe
          275          280          285
Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr
          290          295          300
Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp
305          310          315          320
Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys
          325          330          335
Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met
          340          345          350
Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn
          355          360          365
Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp
          370          375          380
Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
385          390          395          400
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
          405          410          415
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
          420          425          430
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
          435          440          445
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser
          450          455          460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
465          470          475          480
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
          485          490          495
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr
          500          505          510
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser
          515          520          525
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn
530          535          540
Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu
545          550          555          560
Asn Lys Ala Lys Ser
          565

```

```

<210> 12
<211> 566
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> ORF0657nH

```

```

<400> 12

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Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
			35				40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
			115				120						125		
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
			195				200						205		
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
			275				280						285		
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405					410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		

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Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                                440                                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                                455                                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
    465                                470                                475                                480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
    485                                490                                495
Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro
    500                                505                                510
Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly
    515                                520                                525
Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys
    530                                535                                540
Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln
    545                                550                                555                                560
Glu Asn Lys Ala Lys Ser
    565

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<210> 13
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 13
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1                                5                                10                                15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
    20                                25                                30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
    35                                40                                45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
    50                                55                                60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
    65                                70                                75                                80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
    85                                90                                95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
    100                                105                                110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
    115                                120                                125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
    130                                135                                140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
    145                                150                                155                                160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
    165                                170                                175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
    180                                185                                190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
    195                                200                                205

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Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210                               215                               220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225                               230                               235                               240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
                               245                               250                               255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260                               265                               270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
275                               280                               285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290                               295                               300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305                               310                               315                               320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
                               325                               330                               335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
340                               345                               350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
355                               360                               365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
370                               375                               380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
420                               425                               430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
450                               455                               460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                               470                               475                               480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Lys Val Glu Ser Ser
485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
500                               505                               510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
565

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```

<210> 14
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 14

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	
1				5					10					15		
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	
			20					25					30			
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	
		35					40					45				
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	
	50					55					60					
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	
65				70					75						80	
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Glu	
				85					90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	
			100					105					110			
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	
		115				120						125				
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	
	130					135						140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	
145				150						155					160	
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Ala	Ser	Tyr	Asp	Thr	Val	
				165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala	
			180					185					190			
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	
	195					200						205				
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	
	210					215						220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	
225				230						235					240	
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	
				245					250					255		
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	
			260					265					270			
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	
		275					280					285				
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	
	290					295					300					
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	
305					310					315					320	
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	
				325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	
			340					345					350			
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	
	355						360					365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	
	370					375					380					
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	
385					390					395					400	
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	
				405					410					415		

```

Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420                                425                                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                                440                                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                                455                                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
    465                                470                                475                                480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
    485                                490                                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Val Lys
    500                                505                                510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
    515                                520                                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
    530                                535                                540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
    545                                550                                555                                560
Thr Gln Glu Asn Lys Ala Lys Ser
    565

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<210> 15
 <211> 564
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 15
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
    20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
    35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
    50          55          60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile
    65          70          75          80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
    85          90          95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
    100         105         110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
    115         120         125
Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly
    130         135         140
Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp
    145         150         155         160
Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr
    165         170         175
Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile
    180         185         190

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Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr
    195                200                205
Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys
    210                215                220
Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys
    225                230                235                240
Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp
    245                250                255
Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp
    260                265                270
Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe
    275                280                285
Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr
    290                295                300
Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp
    305                310                315                320
Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys
    325                330                335
Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met
    340                345                350
Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn
    355                360                365
Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp
    370                375                380
Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
    385                390                395                400
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
    405                410                415
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
    420                425                430
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
    435                440                445
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser
    450                455                460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
    465                470                475                480
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
    485                490                495
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala
    500                505                510
Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser Ser
    515                520                525
Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr
    530                535                540
Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn
    545                550                555                560
Lys Ala Lys Ser

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<210> 16
<211> 565
<212> PRT
<213> Artificial Sequence

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<220>

<223> ORF0657nH

<400> 16

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	50	55	60	
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	65	70	75	80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	85	90	95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	100	105	110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	115	120	125	
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	130	135	140	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	145	150	155	160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	165	170	175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	180	185	190	
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	195	200	205	
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	210	215	220	
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	225	230	235	240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	245	250	255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	260	265	270	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	275	280	285	
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	290	295	300	
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	305	310	315	320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	325	330	335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Tyr	Trp	Lys	Asp	Phe	Met		340	345	350	
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	355	360	365	
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	370	375	380	
Ala	Ile	Val	Arg	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	385	390	395	400
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp				


```

          405          410          415
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
          420          425          430
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
          435          440          445
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser
          450          455          460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
          465          470          475          480
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
          485          490          495
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr
          500          505          510
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser
          515          520          525
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn
          530          535          540
Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu
          545          550          555          560
Asn Lys Ala Lys Ser
          565

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<210> 17
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 17
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1          5          10          15
Ala Leu Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Thr Lys
          20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
          50          55          60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr
          65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
          145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175

```

Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
 180 185 190
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210 215 220
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225 230 235 240
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
 275 280 285
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
 290 295 300
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
 305 310 315 320
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
 325 330 335
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
 340 345 350
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
 355 360 365
 Ile Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
 370 375 380
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
 385 390 395 400
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
 405 410 415
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
 420 425 430
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
 435 440 445
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
 450 455 460
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
 465 470 475 480
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
 485 490 495
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
 500 505 510
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
 515 520 525
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
 530 535 540
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
 545 550 555 560
 Thr Gln Glu Asn Lys Ala Lys Ser
 565

<210> 18

<211> 565

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 18

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	
1				5					10					15		
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys	
			20					25					30			
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	
		35					40					45				
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	
	50				55						60					
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	
65				70					75						80	
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	
			85					90					95			
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	
		100						105					110			
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	
	115					120						125				
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	
	130					135					140					
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	
145				150					155						160	
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	
			165					170					175			
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	
		180						185					190			
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	
	195					200						205				
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	
	210				215						220					
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	
225				230					235					240		
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	
			245					250					255			
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	
	260					265							270			
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	
	275					280						285				
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	
	290				295						300					
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	
305				310					315					320		
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	
			325					330					335			
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	
	340					345						350				
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	
	355					360						365				
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	
	370					375					380					

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Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr
385                      390                      395                      400
His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp
                      405                      410                      415
Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala
                      420                      425                      430
Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu
435                      440                      445
Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Pro Leu Pro Ser
450                      455                      460
Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr
465                      470                      475                      480
Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr
                      485                      490                      495
Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr
500                      505                      510
Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser
515                      520                      525
Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn
530                      535                      540
Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu
545                      550                      555                      560
Asn Lys Ala Lys Ser
                      565

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<210> 19
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 19
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1      5      10
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
20     25     30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35     40     45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50     55     60
Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65     70     75     80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85     90     95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100    105    110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
115    120    125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130    135    140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145    150    155    160

```

Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	
				165					170						175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	
			180					185						190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	
		195					200					205				
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	
	210					215					220					
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	
	225				230					235					240	
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	
				245					250					255		
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	
			260					265						270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	
		275					280					285				
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	
	290					295					300					
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	
	305				310					315					320	
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	
				325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	
			340				345						350			
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	
	355						360					365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	
	370					375					380					
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	
	385				390					395					400	
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	
			405					410						415		
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	
			420					425					430			
Arg	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	
	435					440						445				
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	
	450					455					460					
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	
	465				470					475					480	
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	
				485				490						495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	
			500					505					510			
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	
	515					520						525				
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	
	530					535					540					
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	
	545				550					555					560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser									
				565												

<210> 20

<211> 568

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> ORF0657nH

<400> 20

Ala 1	Glu	Glu	Thr	Gly 5	Gly	Thr	Asn	Thr	Glu 10	Ala	Gln	Pro	Lys	Thr 15	Glu
Ala 20	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser 25	Glu	Lys	Ala	Pro	Glu 30	Thr	Lys
Pro 35	Val	Ala	Asn	Ala	Val	Ser	Val	Ser 40	Asn	Lys	Glu	Val	Glu 45	Ala	Pro
Thr 50	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu 55	Val	Lys	Glu	Val	Lys 60	Ala	Pro
Lys 65	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala 70	Thr	Lys	Ala	Asp	Asn 75	Asn	Thr 80
Tyr	Pro	Ile	Leu	Asn 85	Gln	Glu	Leu	Arg 90	Glu	Ala	Ile	Lys	Asn 95	Pro	Ala
Ile	Lys	Asp	Lys	Asp 100	His	Ser	Ala	Pro 105	Asn	Ser	Arg	Pro	Ile 110	Asp	Phe
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln 120	Gln	Phe	Tyr	His	Tyr 125	Ala	Ser
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe 135	Thr	Asp	Ser	Lys	Pro 140	Glu	Ile
Glu 145	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe 150	Trp	Arg	Lys	Phe	Glu 155	Val	Tyr 160
Glu	Gly	Asp	Lys	Lys 165	Leu	Pro	Ile	Lys 170	Leu	Val	Ser	Tyr	Asp 175	Thr	Val
Lys	Asp	Tyr	Ala	Tyr 180	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys	Ile	Val	Ser 195	Ser	Thr	His	Phe 200	Asn	Asn	Lys	Glu	Lys 205	Tyr	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln 215	Pro	Ile	Tyr	Asn	Ser 220	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys 230	Ala	Glu	Lys	Leu	Leu 235	Ala	Pro 240
Tyr	Lys	Lys	Ala	Lys 245	Thr	Leu	Glu	Arg 250	Gln	Val	Tyr	Glu	Leu 255	Asn	Lys
Ile	Gln	Asp	Lys	Leu 260	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr	Lys 270	Lys	Lys
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp 280	Glu	Gln	Val	Lys	Ser 285	Ala	Ile
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr 295	Asn	Glu	Lys	Met	Thr 300	Asp	Leu
Gln 305	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu 310	Ser	Val	Glu	Asn	Asn 315	Glu	Ser 320
Met	Met	Asp	Thr	Phe 325	Val	Lys	His	Pro 330	Ile	Lys	Thr	Gly	Met 335	Leu	Asn
Gly	Lys	Lys	Tyr	Met 340	Val	Met	Glu	Thr 345	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val 360	Arg	Thr	Ile	Ser	Lys 365	Asp	Ala

```

Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
  370                               375                               380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
 385                               390                               395                               400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                               405                               410                               415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                               420                               425                               430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                               435                               440                               445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                               450                               455                               460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
 465                               470                               475                               480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                               485                               490                               495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                               500                               505                               510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                               515                               520                               525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
 530                               535                               540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
 545                               550                               555                               560
Thr Gln Glu Asn Lys Ala Lys Ser
                               565

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<210> 21
 <211> 576
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 21
Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
                               20                               25                               30
Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
                               35                               40                               45
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
 50                               55                               60
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
 65                               70                               75                               80
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
                               85                               90                               95
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
                               100                              105                              110
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
                               115                              120                              125
Gln Gln Phe Tyr His Tyr Ala Gly Ser Val Lys Pro Ala Arg Val Ile
 130                              135                              140

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Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	145	150	155	160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	165	170	175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	180	185	190	
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	195	200	205	
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	210	215	220	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	225	230	235	240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	245	250	255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	260	265	270	
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	275	280	285	
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	290	295	300	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	305	310	315	320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	325	330	335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	340	345	350	
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	355	360	365	
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	370	375	380	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	385	390	395	400
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	405	410	415	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys	420	425	430	
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro	435	440	445	
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	450	455	460	
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Gly	Val	Glu	Lys	Glu	Asn	465	470	475	480
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro	485	490	495	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	500	505	510	
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	515	520	525	
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	530	535	540	
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	545	550	555	560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser	565	570	575	

<210> 22
 <211> 576
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 22
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1 5 10 15
 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
 20 25 30
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
 35 40 45
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
 50 55 60
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
 65 70 75 80
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
 85 90 95
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
 100 105 110
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
 115 120 125
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
 130 135 140
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
 145 150 155 160
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
 165 170 175
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
 180 185 190
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
 195 200 205
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
 210 215 220
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
 225 230 235 240
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
 245 250 255
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
 260 265 270
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu
 275 280 285
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
 290 295 300
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
 305 310 315 320
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
 325 330 335
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
 340 345 350

```

Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg
      355                      360                      365
Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile
      370                      375                      380
Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
385                      390                      395                      400
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
      405                      410                      415
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys
      420                      425                      430
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro
      435                      440                      445
Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
      450                      455                      460
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn
465                      470                      475                      480
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
      485                      490                      495
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
      500                      505                      510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
      515                      520                      525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
      530                      535                      540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545                      550                      555                      560
Thr Gln Ser Gln Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
      565                      570                      575

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<210> 23
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 23
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1                      5                      10                      15
Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50                      55                      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65                      70                      75                      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
      85                      90                      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
      100                      105                      110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
      115                      120                      125

```

Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
130						135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asn	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Gly
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ser	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325				330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340				345						350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455				460					
Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Thr	Thr	Lys	Pro	Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser
				485				490						495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Ile	Asp	Val	Val	Gln	Thr	Ser
		515					520					525			
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Glu	Asn	Asn	Lys	Asn
545					550					555					560

Thr Gln Glu Asn Lys Ala Lys Ser
565

<210> 24
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657nH

<400> 24
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1 5 10 15
Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
20 25 30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35 40 45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50 55 60
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65 70 75 80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85 90 95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100 105 110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115 120 125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130 135 140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145 150 155 160
Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
165 170 175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
180 185 190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
195 200 205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210 215 220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro
225 230 235 240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
245 250 255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260 265 270
Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
275 280 285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290 295 300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305 310 315 320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
325 330 335

```

Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340      345      350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
      355      360      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370      375      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385      390      395      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405      410      415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
      450      455      460
Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465      470      475      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
      500      505      510
Pro Thr Thr Ala Ser Ser Glu Thr Thr Thr Ile Asp Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn
545      550      555      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 25
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 25
Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
      20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Ala Ala Pro
      35      40      45
Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50      55      60
Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
      100      105      110

```

Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser		
		115					120					125					
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile		
	130					135					140						
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr		
145					150					155					160		
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val		
				165					170					175			
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala		
			180					185					190				
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr		
	195						200					205					
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp		
	210					215					220						
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro		
225					230					235					240		
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys		
				245					250					255			
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys		
			260					265					270				
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile		
	275						280					285					
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu		
	290					295					300						
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser		
305					310					315					320		
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn		
				325					330					335			
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Asn	Asp	Asp	Tyr	Trp	Lys			
			340				345					350					
Asp	Phe	Met	Val	Glu	Gly	Glu	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala		
	355						360					365					
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr		
	370					375					380						
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp		
385					390					395					400		
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala		
				405					410					415			
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys		
			420					425				430					
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Ala	Pro	Val		
	435						440					445					
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln		
	450					455					460						
Ser	Pro	Ser	Val	Glu	Lys	Glu	Ile	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys		
465					470					475					480		
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser		
				485					490					495			
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Ala	Thr	Gln	Asn	Val	Ala	Lys		
			500					505					510				
Pro	Thr	Ser	Ala	Ser	Ser	Glu	Thr	Thr	Lys	Gly	Val	Val	Gln	Thr	Ser		
	515						520						525				
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Asn	Ala	Pro	Leu	Gln	Lys	Ala	Asn		
	530					535					540						

Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
 545 550 555 560
 Thr Gln Glu Asn Lys Ala Lys Ser
 565

<210> 26
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 26
 Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu
 1 5 10 15
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
 20 25 30
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro
 35 40 45
 Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50 55 60
 Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
 65 70 75 80
 Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
 85 90 95
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
 100 105 110
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
 115 120 125
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
 130 135 140
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
 145 150 155 160
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
 165 170 175
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
 180 185 190
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210 215 220
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225 230 235 240
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
 275 280 285
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
 290 295 300
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
 305 310 315 320

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Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
      325                      330                      335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340                      345                      350
Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala
      355                      360                      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370                      375                      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405                      410                      415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420                      425                      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val
      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
450                      455                      460
Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys
      500                      505                      510
Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser
      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn
530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 27
 <211> 570
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 27
Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys
1      5      10      15
Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu
      20      25      30
Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
35      40      45
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
50      55      60
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
65      70      75      80
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
      85      90      95

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Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	
			100					105					110			
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	
		115					120					125				
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	
		130				135						140				
Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	
145					150					155					160	
Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	
				165					170						175	
Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	
			180					185					190			
Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	
		195					200					205				
Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	
		210				215					220					
Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	
225					230					235					240	
Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	
				245					250						255	
Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	
			260					265					270			
Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	
		275					280					285				
Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	
		290				295					300					
Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	
305					310					315					320	
Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	
				325					330					335		
Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	
			340					345					350			
Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	
		355					360					365				
Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	
		370				375					380					
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	
385					390					395					400	
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	
				405					410					415		
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	
			420					425					430			
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	
		435					440					445				
Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	
		450				455					460					
Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	
465					470					475					480	
Gly	Lys	Gly	Val	Thr	Leu	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	
				485					490					495		
Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	
			500					505					510			
Ala	Lys	Pro	Thr	Thr	Gly	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	
		515					520					525				

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Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys
  530                      535                      540
Ala Asn Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn
  545                      550                      555                      560
Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
                      565                      570

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<210> 28
 <211> 654
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 2 modified to contain a glycine after
 the amino terminus methionine and a carboxyl
 His-Tag

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<400> 28
Met Gly Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg
  1                      5                      10                      15
Lys Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu
  20                      25                      30
Leu Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly
  35                      40                      45
Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr
  50                      55                      60
Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val
  65                      70                      75                      80
Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu
  85                      90                      95
Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val
  100                     105                     110
Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln
  115                     120                     125
Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His
  130                     135                     140
Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp
  145                     150                     155                     160
Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg
  165                     170                     175
Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser
  180                     185                     190
Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu
  195                     200                     205
Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile
  210                     215                     220
Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser
  225                     230                     235                     240
Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu
  245                     250                     255
Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu
  260                     265                     270
Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr
  275                     280                     285

```

```

Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro
 290                               295                 300
Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys
305                               310                 315                 320
Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val
                               325                 330                 335
Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val
                               340                 345                 350
Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val
                               355                 360                 365
Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val
                               370                 375                 380
Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly
385                               390                 395                 400
Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr
                               405                 410                 415
Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val
                               420                 425                 430
Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg
                               435                 440                 445
Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn
                               450                 455                 460
Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala
465                               470                 475                 480
Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys
                               485                 490                 495
Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys
                               500                 505                 510
Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr
                               515                 520                 525
Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys
                               530                 535                 540
Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser
545                               550                 555                 560
Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala
                               565                 570                 575
Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp
                               580                 585                 590
Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala
                               595                 600                 605
Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu
610                               615                 620
Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu
625                               630                 635                 640
Pro Arg Lys Arg Lys Asn Leu Glu His His His His His His
                               645                 650

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<210> 29

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> Full length ORF0657n + Carboxyl His-Tag

<400> 29

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atgaacaaac agcaaaaaga atttaaataca ttttattcaa ttagaaagtc atcactaggc 60
gttgcatctg tagcaattag tacactttta ttattaatgt caaatggcga agcacaagca 120
gcagctgaag aaacaggtgg tacaataaca gaagcacaac caaaaactga agcagttgca 180
agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240
gtatctaata aagaagttga ggcccctact tctgaaacaa aagaagctaa agaagttaaa 300
gaagttaaag cccctaagga acaaaaagaa gttaaaccag cagcaaaagc cactaacaat 360
acataccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagac 420
aaagatcata gcgcacacaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480
actcaacagt tttatcatta tgcaagttct gttaaaccctg ctagagttat tttcactgat 540
tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600
tatgaaggtg acaaaaagtt gccaatataa ttagtatcat acgatactgt taaagattat 660
gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720
cacttcaata acaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780
tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840
ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900
aaacttcctg aaaaattaaa ggctgagtag aagaagaaat tagaggatac aaagaaagct 960
ttagatgagc aagtgaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020
aaaatgactg atttacaaga taaaaatat gttgtttatg aaagtgttga gaataacgaa 1080
tctatgatgg atacttttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140
tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200
cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260
gttgaaggta aaactctata tgatgctatc gttaaagtgc acgtaaaaac gattgattat 1320
gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380
aatctaacaa aaaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440
cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500
gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560
aaagacaaaa cgctgtctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620
ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatacaaa 1680
acaacaaaag atgttgttca aacttcagca gtttctagcg aagcaaaaaga tagtgctcca 1740
ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800
aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860
atgacattac cattaatggc attattagct ttaagtagca tcgttgcatc cgtattacct 1920
agaaaacgta aaaacctcga gcaccaccac caccaccact ga 1962

```

<210> 30

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657nH + Carboxyl His-Tag

<400> 30

```

atgaacgctg aagaaacagtg tggtaacaaat acagaagcac aacccaaaaac tgaagcagtt 60
gcaagtccaa caacaacatc tgaaaaagct ccagaaacta aaccagtagc taatgctgtc 120
tcagtatcta ataaagaagt tgaggcccct acttctgaaa caaaagaagc taaagaagtt 180
aaagaagtta aagcccctaa ggaaacaaaa gaagttaaac cagcagcaaa agccactaac 240
aatacatatc ctattttgaa tcaggaactt agagaagcga ttaaaaaccc tgcaataaaa 300
gacaaagatc atagcgcacc aaactctcgt ccaattgatt ttgaaatgaa aaagaaagat 360
ggaactcaac agttttatca ttatgcaagt tctgttaaac ctgctagagt tattttcact 420
gattcaaaac cagaaattga attaggatta caatcaggtc aattttggag aaaatttgaa 480
gtttatgaag gtgacaaaaa gttgccaatt aaattagtat catacgatac tgttaaagat 540
tatgcttaca ttcgcttctc tgtatcaaac ggaacaaaag ctgttaaaat tgtttagttca 600

```

```

acacacttca ataacaaaga agaaaaatac gattacacat taatggaatt cgcacaacca 660
atttataaca gtgcagataa attcaaaact gaagaagatt ataaagctga aaaattatta 720
gcgccatata aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaacttc ctgaaaaatt aaaggctgag tacaagaaga aattagagga tacaagaaa 840
gcttttagatg agcaagtga atcagctatt actgaattcc aaaatgtaca accaacaat 900
gaaaaaatga ctgatttaca agatacaaaa tatgttgttt atgaaagtgt tgagaataac 960
gaatctatga tggatacttt tgttaaacac cctattaaaa caggatatgt taacggcaaa 1020
aatatatgg tcatggaaac tactaatgac gattactgga aagatttcat ggttgaagg 1080
caacgtgtta gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgatgct atcgttaaag ttcacgtaaa aacgattgat 1200
tatgatggac aataccatgt cagaatcggt gataaagaag catttacaaa agccaatacc 1260
gataaatcta acaaaaaaga acaacaagat aactcagcta agaaggaaagc tactccagct 1320
acgcctagca aaccaacacc atcacctggt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcac tagtgagtca 1440
ggtaaagaca aaacgcctgc taaaaacca actaaagggtg aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatgttgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaaacttca gcaggttcta gcgaagcaaa agatagtgt 1620
ccattacaaa aagcaaacat taaaaacaca aatgatggac acactcaaag ccaaaacaat 1680
aaaaatacac aagaaaataa agcaaaatca ctcgagcacc accaccacca ccactga 1737

```

<210> 31

<211> 1941

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag
and is codon optimized for yeast expression

<400> 31

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgtat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgctg aagaaactgg ttgtaccaac actgaagctc aaccaagac cgaagctgtc 180
gttcccccac cactacctc tgaaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttcta acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagtt 300
aaggaagtca aggtccaaa ggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattg agagaagcta ttaagaacc agctatcaag 420
gacaaggacc actcgcgtcc aaactctaga ccaatcgact tcgaaatgaa gaagaaggac 480
ggtacccaac aattctacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttg caatccggtc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaatt aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttctaac ggtactaagg ctgtcaagat tgtctcttcc 720
accacttca acaacaagga agaaaagtac gactacactt tgatggaatt cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgttg 840
gtccatatac agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagttgc cagaaaagtt gaaggctgaa tacaagaaga agttggaaga caccaagaag 960
gctttggacg aacaagtcaa gtccgctatc accgaattcc aaaacgttca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgtct acgaatccgt cgaaaacaac 1080
gaatccatga tggacacctt cgttaagcac ccaattaaga ctggtatgtt gaacggtaag 1140
aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat ggttgaagg 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctagaacat tatcttccca 1260
tacgttgaag gtaagacttt gtacgacgct atcgtaagg ttcacgtcaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctttcaccaa ggctaacc 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaaagc taccacagct 1440
accccatcta agccaacccc atctccagtt gaaaaggaat ctcaaaagca agactccaa 1500

```

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aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggtaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttcctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgcta agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctggttctt ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacacc aacgacggtc acaccaatc ccaaaacaac 1800
aagaacactc aagaaaacaa ggctaagtct ttgccacaaa ccggtgaaga atccaacaag 1860
gacatgacct tgccattgat ggctttgttg gctttgtctt ccatcgttgc tttcgtcttg 1920
ccaagaaaga gaaagaacta a                                     1941

```

<210> 32

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 3 and is codon optimized for
yeast expression

<400> 32

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agtccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cagttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaacccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggg 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgtcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa                                     1710

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<210> 33

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 1 and is codon optimized for yeast expression

<400> 33

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttaccgcac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatattg ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaaccgt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtcacaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320
ccatctaagc caaccccata a

```

<210> 34

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 34

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttaccgcac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatattg ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaaccgt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

```

```

tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaacg acgcgtcttc tgaatccggg 1440
aagggtgtca ctttggttac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 35

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 35

```

atggctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtoga agtccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttccg acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggtgaaaaa gttgttggt 720
ccatacaaga aggtctaagac ttttgaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaacg acgcgtcttc tgaatccggg 1440
aagggtgtca ctttggttac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```


<210> 36
 <211> 1710
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 7 containing an amino terminus
 methionine and is codon optimized for yeast
 expression

<400> 36
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
 tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
 gtttctaaca aggaagtcga agtccaacc tccgaaacta aggaagctaa ggaagttaag 180
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
 acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtta tttcaccgac 420
 tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
 tacgaaggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
 gcttacatca gattctccgt ttctaaccgt actaaggctg tcaagattgt ctctccacc 600
 cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
 tccatgatgg acaccttctg taagcaccca attagactg gtatgttgaa cggtagaag 1020
 tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
 agagtcagaa ccactccaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
 gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
 gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
 ccactaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
 aagggtgtta ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
 ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ttcttccaag 1560
 actaccaagg acgttgtcca aacttctgct ggttctctctg aagctaagga ctctgtctca 1620
 ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca ccaatccca aaacaacaag 1680
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 37
 <211> 1710
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 7 containing an amino terminus
 methionine and is codon optimized for yeast
 expression

<400> 37
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
 tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
 gtttctaaca aggaagtcga agtccaacc tccgaaacta aggaagctaa ggaagttaag 180

```

gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtag gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtagaaga 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat ctcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaaac acgctgtctc tgaatccggt 1440
aagggcggtta ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa
1710

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<210> 38

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 38

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tcccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtoga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtag gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtagaaga 1020

```

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tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctt tgaatccggt 1440
aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 39

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 39

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttcttaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaa 180
gaagtcaagg ctccaaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctt gtcaagccag cttaggttat ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcgaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctt tgaatccggt 1440
aagggtgtca ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 40

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 40

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatlaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aagggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggtgtta ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct gggtcctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 41

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 41

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240

```

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acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt ggggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caacccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaagacg acgctcttc tgaatccggt 1440
aagggtgta ctttggtctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 42

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI+

<400> 42

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Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
  1          5          10          15
Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
          20          25          30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
          35          40          45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
          50          55          60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
          65          70          75          80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
          85          90          95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
          100          105          110
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
          115          120          125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
          130          135          140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
          145          150          155          160

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Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
      165      170      175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
      180      185      190
Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys
      195      200      205
Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
      210      215      220
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
      225      230      235      240
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
      245      250      255
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
      260      265      270
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
      275      280      285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
      290      295      300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
      305      310      315      320
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
      325      330      335
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
      340      345      350
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
      355      360      365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
      370      375      380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
      385      390      395      400
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
      405      410      415
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
      420      425      430
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro
      435      440      445
Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys
      450      455      460
Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly
      465      470      475      480
Lys

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<210> 43
 <211> 1452
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 42 and is codon optimized for
 yeast expression

<400> 43
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60

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tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtctga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggtgaaaa gttgttggt 720
ccatacaaga aggtcaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaagggt 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggg 1440
aagtaaggat cc 1452

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<210> 44
 <211> 605
 <212> PRT
 <213> ORF0657nG

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<400> 44
Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
  1          5          10          15
Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
          20          25          30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
          35          40          45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
          50          55          60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
          65          70          75          80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
          85          90          95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
          100          105          110
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
          115          120          125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
          130          135          140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
          145          150          155          160
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
          165          170          175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
          180          185          190

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Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	195	200	205
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	210	215	220
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	225	230	235
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	245	250	255
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	260	265	270
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	275	280	285
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	290	295	300
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	305	310	315
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	325	330	335
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	340	345	350
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	355	360	365
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	370	375	380
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	385	390	395
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	405	410	415
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	420	425	430
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	435	440	445
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	450	455	460
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	465	470	475
Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	485	490	495
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	500	505	510
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	515	520	525
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	530	535	540
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	545	550	555
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	565	570	575
Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	580	585	590
Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg	Lys	Arg	Lys	Asn				595	600	605

<210> 45

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 44 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 45

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa tttcacccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttgggttctc acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaacccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat ctcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttctctct aagctaagga ctctgtctca 1620
ttgcaaaaagg ctaacatcaa gaacaccaac gcgggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttg ccacaacccg gtgaagaatc caacaaggac 1740
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1800
agaaagagaa agaactaa                                     1818

```

<210> 46

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 17 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 46

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120

```

```

gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggatttcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatgggtc tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaataacg acgctgtctc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatcca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 47

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 17 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 47

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 60
tcccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggatttcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

```

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tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagtaa 1446

```

<210> 48

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 17 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 48

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 60
tccccaaaca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtta tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatlaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaagaa caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a 1341

```

<210> 49

<211> 1938

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes for full length ORF0657n containing SEQ ID NO: 17 modified to contain a glycine after the amino terminus methionine and is codon optimized for yeast expression

<400> 49

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 180
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 240
gttttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaa 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacgg 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccggccaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttcacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140
tacatgggtc tggaaccac taacgacgac tactggaagg acttcatggt tgaaggctaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatc 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacgggtcaat accacgttag aattgttgac aaggaaagct tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaaa 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccgg 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac taccaaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1740
ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttggct ttgtcttcca tcgttgcttt cgtcttgcca 1920
agaaagagaa agaactaa
1938

```

<210> 50

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 20, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 50

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaa 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacgg 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggccaat tctggagaaa gttcgaagtc 480

```

```

tacgaagggtg acaagaagtt gccaatlaag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgtttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat ctctccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctctctc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 51

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 20 I+ region, is codon
 optimized for yeast expression, and encodes a
 methionine initiation codon

<400> 51

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatlaag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgtttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat ctctccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320

```

```
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaa 1446
```

<210> 52
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes the SEQ ID NO: 20 I region, is codon
 optimized for yeast expression, and encodes a
 methionine initiation codon

```
<400> 52
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtgcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
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tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
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tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
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gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgtag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
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ccatctaagc caaccccata a 1341
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<210> 53
 <211> 1938
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes for full length ORF0657n containing SEQ ID
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 amino terminus methionine and is codon optimized
 for yeast expression

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gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 180
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 240
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acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa ggaaaacgg 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 540
tctaagccag aaatcgattt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 600
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aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
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gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1320
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380
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ccatctaagc caacccatc tccagttgaa aaggaatctc aaaagcaaga ctccaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac taccaaaac gtcgctaagc caactaccgc ttcttccaag 1680
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ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca ccaatcca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
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1938

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<210> 54

<211> 565

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 54

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Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35        40        45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
50        55        60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Thr Tyr Pro Ile
65        70        75        80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
85        90        95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
100       105       110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
115       120       125

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Pro 130	Ala 130	Arg 130	Val 130	Ile 130	Phe 130	Thr 135	Asp 135	Ser 135	Lys 135	Pro 140	Glu 140	Ile 140	Glu 140	Leu 140	Gly 140
Leu 145	Gln 145	Ser 145	Gly 145	Gln 150	Phe 150	Trp 150	Arg 150	Lys 150	Phe 155	Glu 155	Val 155	Tyr 155	Glu 155	Gly 160	Asp 160
Lys 165	Lys 165	Leu 165	Pro 165	Ile 165	Lys 165	Leu 170	Val 170	Ser 170	Tyr 170	Asp 170	Thr 170	Val 170	Lys 170	Asp 175	Tyr 175
Ala 180	Tyr 180	Ile 180	Arg 180	Phe 180	Ser 180	Val 185	Ser 185	Asn 185	Gly 185	Thr 185	Lys 185	Ala 190	Val 190	Lys 190	Ile 190
Val 195	Ser 195	Ser 195	Thr 195	His 195	Phe 200	Asn 200	Asn 200	Lys 200	Glu 200	Glu 205	Lys 205	Tyr 205	Asp 205	Tyr 205	Thr 205
Leu 210	Met 210	Glu 210	Phe 210	Ala 215	Gln 215	Pro 215	Ile 215	Tyr 215	Asn 220	Ser 220	Ala 220	Asp 220	Lys 220	Phe 220	Lys 220
Thr 225	Glu 225	Glu 225	Asp 225	Tyr 230	Lys 230	Ala 230	Glu 230	Lys 230	Leu 235	Leu 235	Ala 235	Pro 235	Tyr 235	Lys 235	Lys 240
Ala 245	Lys 245	Thr 245	Leu 245	Glu 245	Arg 245	Gln 250	Val 250	Tyr 250	Glu 250	Leu 250	Asn 250	Lys 250	Ile 250	Gln 255	Asp 255
Lys 260	Leu 260	Pro 260	Glu 260	Lys 260	Leu 265	Lys 265	Ala 265	Glu 265	Tyr 265	Lys 265	Lys 265	Lys 265	Leu 270	Glu 270	Asp 270
Thr 275	Lys 275	Lys 275	Ala 275	Leu 275	Asp 280	Glu 280	Gln 280	Val 280	Lys 280	Ser 285	Ala 285	Ile 285	Thr 285	Glu 285	Phe 285
Gln 290	Asn 290	Val 290	Gln 290	Pro 295	Thr 295	Asn 295	Glu 295	Lys 295	Met 300	Thr 300	Asp 300	Leu 300	Gln 300	Asp 300	Thr 300
Lys 305	Tyr 305	Ala 305	Val 305	Tyr 310	Glu 310	Ser 310	Val 310	Glu 310	Asn 315	Asn 315	Glu 315	Ser 315	Met 315	Met 315	Asp 315
Thr 320	Phe 320	Val 320	Lys 320	His 325	Pro 325	Ile 325	Lys 325	Thr 325	Gly 330	Met 330	Leu 330	Asn 330	Gly 330	Lys 330	Lys 330
Tyr 340	Met 340	Val 340	Met 340	Glu 340	Thr 340	Thr 345	Asn 345	Asp 345	Asp 345	Tyr 345	Trp 345	Lys 345	Asp 345	Phe 345	Met 345
Val 355	Glu 355	Gly 355	Gln 355	Arg 355	Val 355	Arg 360	Thr 360	Ile 360	Ser 360	Lys 360	Asp 360	Ala 360	Lys 360	Asn 360	Asn 360
Thr 370	Arg 370	Thr 370	Ile 370	Ile 370	Phe 370	Pro 375	Tyr 375	Val 375	Glu 375	Gly 375	Lys 375	Thr 375	Leu 375	Tyr 375	Asp 375
Ala 385	Ile 385	Val 385	Lys 385	Val 385	His 385	Val 390	Lys 390	Thr 390	Ile 390	Asp 390	Tyr 390	Asp 390	Gly 390	Gln 390	Tyr 390
His 405	Val 405	Arg 405	Ile 405	Val 405	Asp 405	Lys 405	Glu 405	Ala 405	Phe 410	Thr 410	Lys 410	Ala 410	Asn 410	Thr 410	Asp 410
Lys 420	Ser 420	Asn 420	Lys 420	Lys 420	Glu 420	Gln 420	Gln 420	Asp 420	Asn 420	Ser 420	Ala 420	Lys 420	Lys 420	Glu 420	Ala 420
Thr 435	Pro 435	Ala 435	Thr 435	Pro 435	Ser 435	Lys 435	Pro 435	Thr 435	Pro 435	Ser 435	Pro 435	Val 435	Glu 435	Lys 435	Glu 435
Ser 450	Gln 450	Lys 450	Gln 450	Asp 450	Ser 450	Gln 450	Lys 450	Asp 450	Asp 450	Asn 450	Lys 450	Gln 450	Leu 450	Pro 450	Ser 450
Val 465	Glu 465	Lys 465	Glu 465	Asn 465	Asp 465	Ala 465	Ser 465	Ser 465	Glu 465	Ser 465	Gly 465	Lys 465	Asp 465	Lys 465	Thr 465
Pro 480	Ala 480	Thr 480	Lys 480	Pro 480	Ala 480	Lys 480	Gly 480	Glu 480	Val 480	Glu 480	Ser 480	Ser 480	Ser 480	Thr 480	Thr 480
Pro 500	Thr 500	Lys 500	Val 500	Val 500	Ser 500	Thr 500	Thr 500	Gln 500	Asn 500	Val 500	Ala 500	Lys 500	Pro 500	Thr 500	Thr 500
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Asn Lys Ala Lys Ser
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<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657nH

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35 40 45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50 55 60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65 70 75 80
Tyr Pro Ile Leu Asn Gln Gly Leu Arg Glu Ala Ile Lys Asn Pro Ala
85 90 95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100 105 110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115 120 125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130 135 140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145 150 155 160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
165 170 175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
180 185 190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
195 200 205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210 215 220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225 230 235 240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
245 250 255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260 265 270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile
275 280 285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290 295 300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305 310 315 320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
325 330 335

Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
 340 345 350
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
 355 360 365
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
 370 375 380
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
 385 390 395 400
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
 405 410 415
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
 420 425 430
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
 435 440 445
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
 450 455 460
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
 465 470 475 480
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
 485 490 495
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
 500 505 510
 Pro Ile Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
 515 520 525
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
 530 535 540
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<210> 56
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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 35 40 45
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50 55 60
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
 65 70 75 80
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu
 85 90 95
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
 100 105 110

Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Asn	Asp	Asp	Tyr	Trp	Lys		340	345	350
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	385	390	395
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	405	410	415
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	420	425	430
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	435	440	445
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	450	455	460
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	465	470	475
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	485	490	495
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Val	Lys	500	505	510
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	515	520	525
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	530	535	540

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 Thr Gln Glu Asn Lys Ala Lys Ser
 565

<210> 57
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<220>
 <223> ORF0657nH

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 35 40 45
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50 55 60
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
 65 70 75 80
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu
 85 90 95
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe
 100 105 110
 Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
 115 120 125
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
 130 135 140
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
 145 150 155 160
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
 165 170 175
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala
 180 185 190
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210 215 220
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225 230 235 240
 Tyr Lys Lys Ala Lys Thr Xaa Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270

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Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
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Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
    290                                295                300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
    305                                310                315                320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
    325                                330                335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
    340                                345                350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
    355                                360                365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
    370                                375                380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
    385                                390                395                400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
    405                                410                415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420                                425                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                                440                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                                455                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
    465                                470                475                480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
    485                                490                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
    500                                505                510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
    515                                520                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
    530                                535                540
Leu Leu Lys Thr His Asp Gly His Thr Gln Ser Gln Asn Ile Lys Asn
    545                                550                555                560
Thr Lys Lys Asp Lys Ala Lys Ser
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<210> 58

<211> 568

<212> PRT

<213> Artificial Sequence

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<223> ORF0657nH

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    20              25              30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
    35              40              45

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Thr 50	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
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Tyr	Pro	Ile	Leu	Asn 85	Gln	Glu	Leu	Arg	Glu 90	Ala	Ile	Lys	Asn	Pro 95	Ala
Ile	Lys	Asp	Lys 100	Asp	His	Ser	Ala	Pro	Asn 105	Ser	Arg	Pro	Ile 110	Asp	Phe
Glu	Met	Lys 115	Lys	Glu	Asn	Gly	Thr 120	Gln	Gln	Phe	Tyr	His 125	Tyr	Ala	Ser
Ser	Val 130	Lys	Pro	Ala	Arg	Val 135	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
Glu 145	Leu	Gly	Leu	Gln 150	Ser	Gly	Gln	Phe	Trp	Arg 155	Lys	Phe	Glu	Val	Tyr 160
Glu	Gly	Asp	Lys 165	Lys	Leu	Pro	Ile	Lys	Leu 170	Val	Ser	Tyr	Asp	Thr 175	Val
Lys	Asp	Tyr	Ala 180	Tyr	Ile	Arg	Phe	Ser 185	Val	Ser	Asn	Gly	Thr 190	Lys	Ala
Val	Lys 195	Ile	Val	Ser	Ser	Thr 200	His	Phe	Asn	Asn	Lys	Glu 205	Glu	Lys	Tyr
Asp	Tyr 210	Thr	Leu	Met	Glu	Phe 215	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
Lys 225	Phe	Lys	Thr	Glu 230	Glu	Asp	Tyr	Lys	Ala	Glu 235	Lys	Leu	Leu	Ala	Pro 240
Tyr	Lys	Lys	Ala 245	Lys	Thr	Leu	Glu	Arg	Gln	Val 250	Tyr	Glu	Leu	Asn 255	Lys
Ile	Gln	Asp	Lys 260	Leu	Pro	Glu	Lys	Leu 265	Lys	Ala	Glu	Tyr	Lys 270	Lys	Lys
Leu	Glu 275	Asp	Thr	Lys	Lys	Ala	Leu 280	Asp	Glu	Gln	Val	Lys 285	Ser	Ala	Ile
Thr 290	Glu	Phe	Gln	Asn	Val 295	Gln	Pro	Thr	Asn	Glu	Lys 300	Met	Thr	Asp	Leu
Gln 305	Asp	Thr	Lys	Tyr 310	Val	Val	Tyr	Glu	Ser	Val 315	Glu	Asn	Asn	Glu	Ser 320
Met	Met	Asp	Thr 325	Phe	Val	Lys	His	Pro	Ile 330	Lys	Thr	Gly	Met	Leu 335	Asn
Gly	Lys	Lys	Tyr 340	Met	Val	Met	Glu	Thr 345	Thr	Asn	Asp	Asp	Tyr 350	Trp	Lys
Asp	Phe 355	Met	Val	Glu	Gly	Gln	Arg 360	Val	Arg	Thr	Ile	Ser 365	Lys	Asp	Ala
Lys 370	Asn	Asn	Thr	Arg	Thr 375	Ile	Ile	Phe	Pro	Tyr	Val 380	Glu	Gly	Lys	Thr
Leu 385	Tyr	Asp	Ala	Ile 390	Val	Lys	Val	His	Val	Lys 395	Thr	Ile	Asp	Tyr	Asp 400
Gly	Gln	Tyr	His 405	Val	Arg	Ile	Val	Asp	Lys 410	Glu	Ala	Phe	Thr	Lys 415	Ala
Asn	Thr 420	Asp	Lys	Ser	Asn	Lys	Lys	Glu 425	Gln	Gln	Asp	Asn	Ser 430	Ala	Lys
Lys	Glu 435	Ala	Thr	Pro	Ala	Thr 440	Pro	Ser	Lys	Pro	Thr 445	Pro	Ser	Pro	Val
Glu 450	Lys	Glu	Ser	Gln	Lys 455	Gln	Asp	Ser	Gln	Lys	Asp 460	Asp	Asn	Lys	Gln
Leu 465	Pro	Ser	Val	Glu 470	Lys	Glu	Asn	Asp	Ala	Ser 475	Ser	Glu	Ser	Gly	Lys 480

```

Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
      545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 59
<211> 567
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 59
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
      35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50      55      60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
      65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
      100     105     110
Glu Met Asn Lys Lys Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
      115     120     125
Ser Ala Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
      130     135     140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
      145     150     155     160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
      165     170     175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
      180     185     190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Asp
      195     200     205
Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys
      210     215     220
Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr
      225     230     235     240
Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile
      245     250     255

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Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu
 260 265 270
 Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr
 275 280 285
 Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln
 290 295 300
 Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met
 305 310 315 320
 Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly
 325 330 335
 Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp
 340 345 350
 Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys
 355 360 365
 Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu
 370 375 380
 Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly
 385 390 395 400
 Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn
 405 410 415
 Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys Lys
 420 425 430
 Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu
 435 440 445
 Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu
 450 455 460
 Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp
 465 470 475 480
 Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser
 485 490 495
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro
 500 505 510
 Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala
 515 520 525
 Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile
 530 535 540
 Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr
 545 550 555 560
 Gln Glu Asn Lys Ala Lys Ser
 565

<210> 60

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 60

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1 5 10 15
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
 20 25 30

Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys
		35					40					45			
Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys
	50					55					60				
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro
65					70					75					80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
				85					90					95	
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
			100					105					110		
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr
		115					120					125			
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
	130					135					140				
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
				165					170					175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
			180					185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200					205			
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
	210					215					220				
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225					230					235					240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
				245					250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
			260					265					270		
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280					285			
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
	290					295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Ala	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
				325					330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
			340					345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				
Phe	Pro	Tyr	Val	Glu	Gly	Lys									

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Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn
465                               470                               475                               480
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
                               485                               490                               495
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
                               500                               505                               510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
                               515                               520                               525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
                               530                               535                               540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545                               550                               555                               560
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
                               565                               570                               575

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<210> 61
 <211> 572
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 61
Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
                               20                               25                               30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala
                               35                               40                               45
Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu
 50                               55                               60
Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala
65                               70                               75                               80
Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile
                               85                               90                               95
Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg
                               100                              105                              110
Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr
                               115                              120                              125
His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser
130                              135                              140
Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys
145                              150                              155                              160
Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser
                               165                              170                              175
Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn
                               180                              185                              190
Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys
                               195                              200                              205
Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr
210                              215                              220
Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys
225                              230                              235                              240

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Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr
      245      250      255
Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu
      260      265      270
Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val
      275      280      285
Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys
      290      295      300
Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu
305      310      315      320
Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr
      325      330      335
Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp
      340      345      350
Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile
      355      360      365
Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Cys Val
      370      375      380
Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr
385      390      395      400
Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala
      405      410      415
Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp
      420      425      430
Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr
      435      440      445
Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp
      450      455      460
Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser
465      470      475      480
Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu
      485      490      495
Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln
      500      505      510
Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val
      515      520      525
Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu
      530      535      540
Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln
545      550      555      560
Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
      565      570

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<210> 62
 <211> 572
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 62
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1 5 10 15

Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
		35					40					45			
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu
	50					55					60				
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala
65					70					75					80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile
			85						90					95	
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg
			100					105					110		
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr
		115					120					125			
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser
	130					135					140				
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys
145					150					155					160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser
				165					170					175	
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn
			180					185					190		
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys
		195					200					205			
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr
	210					215					220				
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys
225					230					235					240
Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr
				245					250					255	
Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu
		260						265					270		
Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val
		275					280					285			
Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys
	290					295					300				
Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu
305				310						315					320
Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr
				325					330					335	
Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp
			340					345					350		
Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile
		355					360					365			
Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val
	370					375					380				
Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr
385					390					395					400
Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala
				405					410					415	
Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys	Glu	Gln	Gln	Asp
			420					425					430		
Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro	Ser	Lys	Pro	Thr
		435					440					445			

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Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp
  450                               455                               460
Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser
465                               470                               475                               480
Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu
                               485                               490                               495
Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln
                               500                               505                               510
Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val
                               515                               520                               525
Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu
                               530                               535                               540
Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln
545                               550                               555                               560
Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
                               565                               570

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<210> 63
<211> 566
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 63
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1                               5                               10                               15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
                               20                               25                               30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala
                               35                               40                               45
Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu
                               50                               55                               60
Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro
65                               70                               75                               80
Ile Leu Asn Lys Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys
                               85                               90                               95
Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met
                               100                               105                               110
Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val
                               115                               120                               125
Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu
                               130                               135                               140
Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly
145                               150                               155                               160
Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp
                               165                               170                               175
Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys
                               180                               185                               190
Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr
                               195                               200                               205
Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe
210                               215                               220

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Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys
225                230                235                240
Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln
                245                250                255
Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu
                260                265                270
Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu
                275                280                285
Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp
290                295                300
Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met
305                310                315                320
Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys
                325                330                335
Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe
                340                345                350
Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn
                355                360                365
Asn Thr Arg Thr Ile Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr
370                375                380
Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln
385                390                395                400
Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala
                405                410                415
Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu
                420                425                430
Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val Glu Lys
                435                440                445
Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Thr Gln Ser Pro
450                455                460
Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys
465                470                475                480
Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr
                485                490                495
Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr
                500                505                510
Thr Ala Ser Ser Glu Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly
                515                520                525
Pro Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys
530                535                540
Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln
545                550                555                560
Glu Asp Lys Ala Lys Ser
                565

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<210> 64

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> His-Tag

<400> 64

Leu Glu His His His His His His
 1 5

<210> 65
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 65
 ctggccgctcg ttttac 16

<210> 66
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 66
 caggaaacag ctatgac 17

<210> 67
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 67
 aaccggtttt ccatggggaa caaacagcaa aaagaattt 39

<210> 68
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 68
 accggtttct cgaggttttt acgttttcta ggtaatac 38

<210> 69
 <211> 109
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 69
 atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
 ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacg 109

<210> 70
 <211> 110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 70
 gttggggaag cgacagcttc ggtctttggt tgagcttcag tgttggtacc accagtttct 60
 tcagcagcag cttgagcttc accgtagac atcaacaaca acaagggtga 110

<210> 71
 <211> 110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 71
 agaccgaagc tgtcgcttcc ccaaccacta cctctgaaaa ggctccagaa actaagccag 60
 ttgctaacgc tgtctccggt tctaacaagg aagtcgaagc tccaacctcc 110

<210> 72
 <211> 109
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 72
 tggtagcctt agcagctggc ttgacttcct tagtttcctt tggagccttg acttccttaa 60
 cttccttagc ttccttagtt tcggaggttg gagcttcgac ttccttggt 109

<210> 73
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 73
 aagtcaagcc agctgctaag gctaccaaca acacttacct aattttgaac caagaattga 60
 gagaagctat taagaaccca gctatcaagg acaaggacca ctccgctc 108

<210> 74
 <211> 109

<212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 74
 tggcttgaca gaggacgcgt agtggtagaa ttgttgggta ccgtccttct tcttcatttc 60
 gaagtcgatt ggtctagagt ttggagcgga gtggtccttg tccttgata 109

<210> 75
 <211> 102
 <212> DNA
 <213> Artificial Sequence

<220>
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 tcgaattggg ttgcaatcc ggtcaattct ggagaaagtt cg 102

<210> 76
 <211> 104
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 76
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 tcaccttcgt agacttcgaa cttctccag aattgaccgg attg 104

<210> 77
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<220>
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 gattgtctct tccacccact tcaacaacaa ggaagaaaag tacgactac 109

<210> 78
 <211> 109
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 78

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 tgagcgaatt ccatcaaagt gtagtcgtac ttttcttcct tgttggtga 109

<210> 79
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 <213> Artificial Sequence

<220>
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<400> 79
 ccgaagaaga ctacaaggct gaaaagtgtg ttggtccata caagaaggct aagactttgg 60
 aaagacaagt ttacgaattg aacaagatcc aagacaagtt gccaga 106

<210> 80
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 <212> DNA
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<220>
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<400> 80
 tcggtgatag cggacttgac ttgttcgtcc aaagccttct tgggtgtcttc caacttcttc 60
 ttgtattcag ccttcaactt ttctggcaac ttgtcttgga tcttggtca 109

<210> 81
 <211> 109
 <212> DNA
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<400> 81
 cgaacaagtc aagtcgcta tcaccgaatt ccaaaacggt caaccaacta acgaaaagat 60
 gactgacttg caagacacta agtacgtcgt ctacgaatcc gtcgaaaac 109

<210> 82
 <211> 109
 <212> DNA
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<400> 82
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 aggtgtccat catggattcg ttgttttcga cggattcgta gacgacgta 109

<210> 83
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 <212> DNA
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<220>
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'ggttgaaggt caaagagtca gaaccatctc caaggacgct aagaacaac          109

<210> 84
<211> 101
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<400> 84
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ataatgggtc tagtggtggt ctagcgtcc ttggagatgg t          101

<210> 85
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tgttgacaag gaagctttca ccaaggctaa caccgacaag tccaac          106

<210> 86
<211> 96
<212> DNA
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ttccttcttg ttggacttgt cggtgtagc cttggt          96

<210> 87
<211> 85
<212> DNA
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<220>
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<400> 87
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cccaaaagga cgacaacaag caatt          85

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<210> 88
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 <212> DNA
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<220>
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<400> 88
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 tcgacggatg gcaattgctt gttgtcgtcc ttttgggagt 100

<210> 89
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<220>
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<400> 89
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 aaccaaggtt gtctccacta cccaaaacgt cgctaagcca a 101

<210> 90
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 <213> Artificial Sequence

<220>
 <223> ORF0657n oligomer

<400> 90
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 ggaagaagcg gtagttggct tagcgacgtt ttgggtagtg g 101

<210> 91
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 <212> DNA
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<400> 91
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 gacggtcaca cccaatccca aaacaacaag a 91

<210> 92
 <211> 98
 <212> DNA
 <213> Artificial Sequence

<220>

<223> ORF0657n oligomer

<400> 92

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tcgttgcttt cgtcttgcca agaaagagaa agaactaa 98

<210> 93

<211> 98

<212> DNA

<213> Artificial Sequence

<220>

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<400> 93

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<210> 94

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 94

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<210> 95

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 95

tgataagctt gctcaatggc tctcttcctc 30

<210> 96

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 96

aaccggtttg gatccacaaa aacaaaatgg gtaacaagca acaaaaggaa ttc 53

<210> 97

<211> 42

<212> DNA

<213> Artificial Sequence

<220>
 <223> Primer

 <400> 97
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 <210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 98
 gctgaagaaa ctggtggtac caac 24

 <210> 99
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 <220>
 <223> Primer

 <400> 99
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 <210> 100
 <211> 41
 <212> DNA
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 <220>
 <223> Primer

 <400> 100
 ggggggatcc cacaaaacaa aatggctgaa gaaactggtg g 41

 <210> 101
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 101
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 <210> 102
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 102

gggggggatcc cacaaaacaa aatggctgaa gaaactggtg g

41

<210> 103

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 103

gggggggatc cttagttctt tctctttctt gg

32

<210> 104

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 104

ctccggatcc cacaaaacaa aatggctgaa gaaactggt

39

<210> 105

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 105

gctgccggga tccttatggg gttggcttag atggggta

38

<210> 106

<211> 644

<212> PRT

<213> S. aureus

<400> 106

Met	Asn	Lys	Gln	Gln	Lys	Glu	Phe	Lys	Ser	Phe	Tyr	Ser	Ile	Arg	Lys
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Ser	Ser	Leu	Gly	Val	Ala	Ser	Val	Ala	Ile	Ser	Thr	Leu	Leu	Leu	Leu
		20						25				30			
Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn
		35					40					45			
Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Leu	Ala	Ser	Pro	Thr	Thr	Thr
	50					55					60				

Thr	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	65	70	75	80
Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	85	90	95	
Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	100	105	110	
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	115	120	125	
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	130	135	140	
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	145	150	155	160
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	165	170	175	
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	180	185	190	
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	195	200	205	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	210	215	220	
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	225	230	235	240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	245	250	255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	260	265	270	
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	275	280	285	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	290	295	300	
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	305	310	315	320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	325	330	335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	340	345	350	
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	355	360	365	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	370	375	380	
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	385	390	395	400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Ile	Asn	Asn	Thr	Arg	Thr	Ile	Ile	405	410	415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	420	425	430	
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	435	440	445	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	450	455	460	
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	465	470	475	480
Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	485	490	495	

Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn
 500 505 510
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
 515 520 525
 Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
 530 535 540
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr
 545 550 555 560
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
 565 570 575
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
 580 585 590
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
 595 600 605
 Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu
 610 615 620
 Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg
 625 630 635 640
 Lys Arg Lys Asn

<210> 107
 <211> 644
 <212> PRT
 <213> S. aureus

<400> 107
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 20 25 30
 Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn
 35 40 45
 Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr
 50 55 60
 Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val
 65 70 75 80
 Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys
 85 90 95
 Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro
 100 105 110
 Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
 115 120 125
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
 130 135 140
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu
 145 150 155 160
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
 165 170 175
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
 180 185 190
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
 195 200 205

Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
210						215					220				
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
225					230					235					240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
				245					250					255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
			260					265					270		
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
		275					280					285			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
	290					295					300				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu
305					310					315					320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
				325					330					335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
			340					345					350		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
		355					360					365			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
	370					375					380				
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
385					390					395					400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
				405					410					415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
			420					425					430		
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
		435					440					445			
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys
	450					455				460					
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro
465					470					475					480
Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
				485					490					495	
Ser	Gln	Lys	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	
			500				505					510			
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro
		515					520					525			
Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
		530				535					540				
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr
545					550					555					560
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
				565					570					575	
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
			580					585					590		
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
			595				600					605			
Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu
	610					615					620				
Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg
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Lys	Arg	Lys	Asn												

<210> 108
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<220>
<223> cell wall sorting signal

<220>
<221> SITE
<222> 3
<223> Xaa = any amino acid

<400> 108
Leu Pro Xaa Thr Gly
1 5

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> 3
<223> Xaa = any amino acid

<400> 109
Leu Pro Xaa Thr Gly Val Ile
1 5